AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning at page 12, line 14, with the following rewritten paragraph:

--The homology of amino acid sequences or nucleotide sequences can be determined by, for example, algorithm BLAST (Proc. Natl. Acad. Sci. U.S.A. 90: 5873-5877, 1993) according to Karlin and Altschul. Based on this algorithm, a program called BLASTN or a program called BLASTX has been developed (Altschul et al., J. Mol. Biol. 215: 403-410, 1990). When nucleotide sequences are analyzed by BLASTN based on BLAST, parameters are determined to be, for example, score = 100 and word length = 12. Furthermore, when amino acid sequences are analyzed by BLASTX based on BLAST, parameters are determined to be, for example, score = 50 and word length = 3. When BLAST and Gapped BLAST programs are used, default parameters for each program are used. Specific techniques for these analysis methods are known (http://www.ncbi.nlm.nih.gov.).--

GMM/LTP/cjw